



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

10/517,333

Source:

PCT

Date Processed by STIC:

12-22-04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebs/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04



PCT

RAW SEQUENCE LISTING

DATE: 12/22/2004

PATENT APPLICATION: US/10/517,333

TIME: 08:53:36

Input Set : A:\ISPT1011.ST25.txt

Output Set: N:\CRF4\12222004\J517333.raw

3 <110> APPLICANT: Baker, Brenda F.
 4 Freier, Susan M.
 5 Dobie, Kenneth W.
 7 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF IL-1 RECEPTOR-ASSOCIATED KINASE-1
 8 EXPRESSION
 10 <130> FILE REFERENCE: ISPT-1011
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/517,333
 C--> 12 <141> CURRENT FILING DATE: 2004-12-09
 12 <150> PRIOR APPLICATION NUMBER: PCT/US03/18003
 13 <151> PRIOR FILING DATE: 2003-06-09
 15 <150> PRIOR APPLICATION NUMBER: US 10/167,034
 16 <151> PRIOR FILING DATE: 2002-06-10
 18 <160> NUMBER OF SEQ ID NOS: 143
 20 <170> SOFTWARE: PatentIn version 3.3
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 23 <211> LENGTH: 20
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Artificial
 27 <220> FEATURE:
 28 <223> OTHER INFORMATION: Antisense Oligonucleotide
 30 <400> SEQUENCE: 1
 31 tccgtcatcg ctcttcaggg 20
 34 <210> SEQ ID NO: 2
 35 <211> LENGTH: 20
 36 <212> TYPE: DNA
 37 <213> ORGANISM: Artificial
 39 <220> FEATURE:
 40 <223> OTHER INFORMATION: Antisense Oligonucleotide
 42 <400> SEQUENCE: 2
 43 gtgcgcgcga gcccgaatc 20
 46 <210> SEQ ID NO: 3
 47 <211> LENGTH: 20
 48 <212> TYPE: DNA
 49 <213> ORGANISM: Artificial
 51 <220> FEATURE:
 52 <223> OTHER INFORMATION: Antisense Oligonucleotide
 54 <400> SEQUENCE: 3
 55 atgcattctg cccccaagga 20
 58 <210> SEQ ID NO: 4
 59 <211> LENGTH: 3590
 60 <212> TYPE: DNA
 61 <213> ORGANISM: Homo sapiens
 64 <220> FEATURE:

(pg. 6-8) ↖

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68 <400> SEQUENCE: 4
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72 Met Ala Gly Gly Pro Gly Pro Gly Glu Pro Ala
73 1 5 10
75 gcc ccc gcc gcc cag cac ttc ttg tac gag gtg ccg ccc tgg gtc atg 160
76 Ala Pro Gly Ala Gln His Phe Leu Tyr Glu Val Pro Pro Trp Val Met
77 15 20 25
79 tgc cgc ttc tac aaa gtg atg gac gcc ctg gag ccc gcc gac tgg tgc 208
80 Cys Arg Phe Tyr Lys Val Met Asp Ala Leu Glu Pro Ala Asp Trp Cys
81 30 35 40
83 cag ttc gcc gcc ctg atc gtg cgc gac cag acc gag ctg cgg ctg tgc 256
84 Gln Phe Ala Ala Leu Ile Val Arg Asp Gln Thr Glu Leu Arg Leu Cys
85 45 50 55
87 gag cgc tcc ggg cag cgc acg gcc agc gtc ctg tgg ccc tgg atc aac 304
88 Glu Arg Ser Gly Gln Arg Thr Ala Ser Val Leu Trp Pro Trp Ile Asn
89 60 65 70 75
91 cgc aac gcc cgt gtg gcc gac ctc gtg cac atc ctc acg cac ctg cag 352
92 Arg Asn Ala Arg Val Ala Asp Leu Val His Ile Leu Thr His Leu Gln
93 80 85 90
95 ctg ctc cgt gcg cgg gac atc atc aca gcc tgg cac cct ccc gcc ccg 400
96 Leu Leu Arg Ala Arg Asp Ile Ile Thr Ala Trp His Pro Pro Ala Pro
97 95 100 105
99 ctt ccg tcc cca gcc acc act gcc ccg agg ccc agc agc atc cct gca 448
100 Leu Pro Ser Pro Gly Thr Thr Ala Pro Arg Pro Ser Ser Ile Pro Ala
101 110 115 120
103 ccc gcc gag gcc gag gcc tgg agc ccc cgg aag ttg cca tcc tca gcc 496
104 Pro Ala Glu Ala Glu Ala Trp Ser Pro Arg Lys Leu Pro Ser Ser Ala
105 125 130 135
107 tcc acc ttc ctc tcc cca gct ttt cca gcc tcc cag acc cat tca ggg 544
108 Ser Thr Phe Leu Ser Pro Ala Phe Pro Gly Ser Gln Thr His Ser Gly
109 140 145 150 155
111 cct gag ctc gcc ctg gtt cca agc cct gct tcc ctg tgg cct cca ccg 592
112 Pro Glu Leu Gly Leu Val Pro Ser Pro Ala Ser Leu Trp Pro Pro
113 160 165 170
115 cca tct cca gcc cct tct tct acc aag cca gcc cca gag agc tca gtg 640
116 Pro Ser Pro Ala Pro Ser Ser Thr Lys Pro Gly Pro Glu Ser Ser Val
117 175 180 185
119 tcc ctc ctg cag gga gcc cgc ccc tct ccg ttt tgc tgg ccc ctc tgt 688
120 Ser Leu Leu Gln Gly Ala Arg Pro Ser Pro Phe Cys Trp Pro Leu Cys
121 190 195 200
123 gag att tcc cgg gcc acc cac aac ttc tcg gag gag ctc aag atc ggg 736
124 Glu Ile Ser Arg Gly Thr His Asn Phe Ser Glu Glu Leu Lys Ile Gly
125 205 210 215
127 gag ggt gcc ttt ggg tgc gtg tac cgg gcg gtg atg agg aac acg gtg 784
128 Glu Gly Gly Phe Gly Cys Val Tyr Arg Ala Val Met Arg Asn Thr Val
129 220 225 230 235

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131	tat	gct	gtg	aag	agg	ctg	aag	gag	aac	gct	gac	ctg	gag	tgg	act	gca	832
132	Tyr	Ala	Val	Lys	Arg	Leu	Lys	Glu	Asn	Ala	Asp	Leu	Glu	Trp	Thr	Ala	
133				240					245					250			
135	gtg	aag	cag	agc	ttc	ctg	acc	gag	gtg	gag	cag	ctg	tcc	agg	ttt	cgt	880
136	Val	Lys	Gln	Ser	Phe	Leu	Thr	Glu	Val	Glu	Gln	Leu	Ser	Arg	Phe	Arg	
137				255				260						265			
139	cac	cca	aac	att	gtg	gac	ttt	gct	ggc	tac	tgt	gct	cag	aac	ggc	ttc	928
140	His	Pro	Asn	Ile	Val	Asp	Phe	Ala	Gly	Tyr	Cys	Ala	Gln	Asn	Gly	Phe	
141				270				275						280			
143	tac	tgc	ctg	gtg	tac	ggc	ttc	ctg	ccc	aac	ggc	tcc	ctg	gag	gac	cgt	976
144	Tyr	Cys	Leu	Val	Tyr	Gly	Phe	Leu	Pro	Asn	Gly	Ser	Leu	Glu	Asp	Arg	
145				285				290						295			
147	ctc	cac	tgc	cag	acc	cag	gcc	tgc	cca	cct	ctc	tcc	tgg	cct	cag	cga	1024
148	Leu	His	Cys	Gln	Thr	Gln	Ala	Cys	Pro	Pro	Leu	Ser	Trp	Pro	Gln	Arg	
149	300					305					310					315	
151	ctg	gac	atc	ctt	ctg	ggt	aca	gcc	cgg	gca	att	cag	ttt	cta	cat	cag	1072
152	Leu	Asp	Ile	Leu	Leu	Gly	Thr	Ala	Arg	Ala	Ile	Gln	Phe	Leu	His	Gln	
153					320					325						330	
155	gac	agc	ccc	agc	ctc	atc	cat	gga	gac	atc	aag	agt	tcc	aac	gtc	ctt	1120
156	Asp	Ser	Pro	Ser	Leu	Ile	His	Gly	Asp	Ile	Lys	Ser	Ser	Asn	Val	Leu	
157				335				340							345		
159	ctg	gat	gag	agg	ctg	aca	ccc	aag	ctg	gga	gac	ttt	ggc	ctg	gcc	cgg	1168
160	Leu	Asp	Glu	Arg	Leu	Thr	Pro	Lys	Leu	Gly	Asp	Phe	Gly	Leu	Ala	Arg	
161				350				355						360			
163	ttc	agc	cgc	ttt	gcc	ggg	tcc	agc	ccc	agc	cag	agc	agc	atg	gtg	gcc	1216
164	Phe	Ser	Arg	Phe	Ala	Gly	Ser	Ser	Pro	Ser	Gln	Ser	Ser	Met	Val	Ala	
165				365				370						375			
167	cgg	aca	cag	aca	gtg	cgg	ggc	acc	ctg	gcc	tac	ctg	ccc	gag	gag	tac	1264
168	Arg	Thr	Gln	Thr	Val	Arg	Gly	Thr	Leu	Ala	Tyr	Leu	Pro	Glu	Glu	Tyr	
169	380					385					390					395	
171	atc	aag	acg	gga	agg	ctg	gct	gtg	gac	acg	gac	acc	ttc	agc	ttt	ggg	1312
172	Ile	Lys	Thr	Gly	Arg	Leu	Ala	Val	Asp	Thr	Asp	Thr	Phe	Ser	Phe	Gly	
173					400					405						410	
175	gtg	gta	gtg	cta	gag	acc	ttg	gct	ggt	cag	agg	gct	gtg	aag	acg	cac	1360
176	Val	Val	Val	Leu	Glu	Thr	Leu	Ala	Gly	Gln	Arg	Ala	Val	Lys	Thr	His	
177					415					420						425	
179	ggt	gcc	agg	acc	aag	tat	ctg	aaa	gac	ctg	gtg	gaa	gag	gag	gct	gag	1408
180	Gly	Ala	Arg	Thr	Lys	Tyr	Leu	Lys	Asp	Leu	Val	Glu	Glu	Glu	Ala	Glu	
181				430				435						440			
183	gag	gct	gga	gtg	gct	ttg	aga	agc	acc	cag	agc	aca	ctg	caa	gca	ggt	1456
184	Glu	Ala	Gly	Val	Ala	Leu	Arg	Ser	Thr	Gln	Ser	Thr	Leu	Gln	Ala	Gly	
185				445				450						455			
187	ctg	gct	gca	gat	gcc	tgg	gct	gct	ccc	atc	gcc	atg	cag	atc	tac	aag	1504
188	Leu	Ala	Ala	Asp	Ala	Trp	Ala	Ala	Pro	Ile	Ala	Met	Gln	Ile	Tyr	Lys	
189	460					465					470					475	
191	aag	cac	ctg	gac	ccc	agg	ccc	ggg	ccc	tgc	cca	cct	gag	ctg	ggc	ctg	1552
192	Lys	His	Leu	Asp	Pro	Arg	Pro	Gly	Pro	Cys	Pro	Pro	Glu	Leu	Gly	Leu	
193					480					485						490	
195	ggc	ctg	ggc	cag	ctg	gcc	tgc	tgc	tgc	ctg	cac	cgc	cgg	gcc	aaa	agg	1600

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196	Gly	Leu	Gly	Gln	Leu	Ala	Cys	Cys	Cys	Leu	His	Arg	Arg	Ala	Lys	Arg	
197				495					500					505			
199	agg	cct	cct	atg	acc	cag	gtg	tac	gag	agg	cta	gag	aag	ctg	cag	gca	1648
200	Arg	Pro	Pro	Met	Thr	Gln	Val	Tyr	Glu	Arg	Leu	Glu	Lys	Leu	Gln	Ala	
201			510					515					520				
203	gtg	gtg	gcg	ggg	gtg	ccc	ggg	cat	ttg	gag	gcc	gcc	agc	tgc	atc	ccc	1696
204	Val	Val	Ala	Gly	Val	Pro	Gly	His	Leu	Glu	Ala	Ala	Ser	Cys	Ile	Pro	
205		525					530				535						
207	cct	tcc	ccg	cag	gag	aac	tcc	tac	gtg	tcc	agc	act	ggc	aga	gcc	cac	1744
208	Pro	Ser	Pro	Gln	Glu	Asn	Ser	Tyr	Val	Ser	Ser	Thr	Gly	Arg	Ala	His	
209	540					545					550				555		
211	agt	ggg	gct	gct	cca	tgg	cag	ccc	ctg	gca	gcg	cca	tca	gga	gcc	agt	1792
212	Ser	Gly	Ala	Ala	Pro	Trp	Gln	Pro	Leu	Ala	Ala	Pro	Ser	Gly	Ala	Ser	
213				560					565					570			
215	gcc	cag	gca	gca	gag	cag	ctg	cag	aga	ggc	ccc	aac	cag	ccc	gtg	gag	1840
216	Ala	Gln	Ala	Ala	Glu	Gln	Leu	Gln	Arg	Gly	Pro	Asn	Gln	Pro	Val	Glu	
217			575					580			585						
219	agt	gac	gag	agc	cta	ggc	ggc	ctc	tct	gct	gcc	ctg	cgc	tcc	tgg	cac	1888
220	Ser	Asp	Glu	Ser	Leu	Gly	Gly	Leu	Ser	Ala	Ala	Leu	Arg	Ser	Trp	His	
221		590					595				600						
223	ttg	act	cca	agc	tgc	cct	ctg	gac	cca	gca	ccc	ctc	agg	gag	gcc	ggc	1936
224	Leu	Thr	Pro	Ser	Cys	Pro	Leu	Asp	Pro	Ala	Pro	Leu	Arg	Glu	Ala	Gly	
225		605				610					615						
227	tgt	cct	cag	ggg	gac	acg	gca	gga	gaa	tcg	agc	tgg	ggg	agt	ggc	cca	1984
228	Cys	Pro	Gln	Gly	Asp	Thr	Ala	Gly	Glu	Ser	Ser	Trp	Gly	Ser	Gly	Pro	
229	620				625				630						635		
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232	Gly	Ser	Arg	Pro	Thr	Ala	Val	Glu	Gly	Leu	Ala	Leu	Gly	Ser	Ser	Ala	
233				640					645					650			
235	tca	tcg	tcg	tca	gag	cca	ccg	cag	att	atc	atc	aac	cct	gcc	cga	cag	2080
236	Ser	Ser	Ser	Ser	Glu	Pro	Pro	Gln	Ile	Ile	Ile	Asn	Pro	Ala	Arg	Gln	
237			655				660				665						
239	aag	atg	gtc	cag	aag	ctg	gcc	ctg	tac	gag	gat	ggg	gcc	ctg	gac	agc	2128
240	Lys	Met	Val	Gln	Lys	Leu	Ala	Leu	Tyr	Glu	Asp	Gly	Ala	Leu	Asp	Ser	
241		670					675				680						
243	ctg	cag	ctg	ctg	tcg	tcc	agc	tcc	ctc	cca	ggc	ttg	ggc	ctg	gaa	cag	2176
244	Leu	Gln	Leu	Leu	Ser	Ser	Ser	Leu	Pro	Gly	Leu	Gly	Leu	Glu	Gln		
245		685				690					695						
247	gac	agg	cag	ggg	ccc	gaa	gaa	agt	gat	gaa	ttt	cag	agc	tga			2218
248	Asp	Arg	Gln	Gly	Pro	Glu	Glu	Ser	Asp	Glu	Phe	Gln	Ser				
249	700				705				710								
251	tgtgtttcacc	tgggcagatc	ccccaaatcc	ggaagtcaaa	gtttctcatgg	tcagaagttc											2278
253	tcattggtgca	cgagtctctca	gcactctgcc	ggcagtgggg	gtggggggccc	atgcccgcgg											2338
255	gggagagaag	gaggtggccc	tgctgttcta	ggctctgtgg	gcataggcag	gcagagtggga											2398
257	accctgcctc	catgccagca	tctgggggca	aggaaggctg	gcatcatcca	gtgaggaggc											2458
259	tgggcgcatgt	tgggaggctg	ctggctgcac	agacccgtga	ggggaggaga	ggggctgctg											2518
261	tgcaggggtg	tggagtaggg	agctggctcc	cctgagagcc	atgcagggcg	tctgcagccc											2578
263	aggcctctgg	cagcagctct	ttgccatct	ctttggacag	tggccaccct	gcacaatggg											2638
265	gccgacgagg	cctagggccc	tcctacctgc	ttacaatttg	gaaaagtgtg	gccgggtgcg											2698

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Output Set: N:\CRF4\12222004\J517333.raw

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267 gtggctcacg cctgtaatcc cagcactttg ggaggccaag gcaggaggat cgctggagcc 2758
269 cagtaggtca agaccagcca gggcaacatg atgagaccct gtctctgcc aaaaattttt 2818
271 taaactatta gcctggcggtg gtagcgacac cctgtggtcc cagctgctgg ggaggctgaa 2878
273 gtaggaggat ctttatgct tgggaggtcg aggctgcagt gagtcatgat tgtatgactg 2938
275 cactccagcc tgggtgacag agcaagaccc tgtttcaaaa agaaaaaacc tgggaaaagt 2998
277 gaagtatggc tgtaagtctc atggttcagt cctagcaaga agcgagaatt ctgagatcct 3058
279 ccagaaaagtc gagcagcacc cacctccaac ctccggccag tgtcttcagg ctttactggg 3118
281 gacctgcgag ctggcctaata gtggtggcct gcaagccagg ccatccctgg gcgccacaga 3178
283 cgagctccga gccaggctcag gcttcggagg ccacaagctc agcctcaggc ccaggcactg 3238
285 attgtggcag agggggccact acccaaggct tagctaggcc caagacctag ttaccagac 3298
287 agtgagaagc ccctggaagg cagaaaagtt gggagcatgg cagacaggga agggaaacat 3358
289 tttcaggga aagacatgta tcacatgtct tcagaagcaa gtcagggtttc atgtaaccga 3418
291 gtgtcctctt gcgtgtccaa aagtagccca gggctgtagc acaggcttca cagtgatttt 3478
293 gtgttcagcc gtgagtcaca ctacatgccc ccgtgaagct gggcattggt gacgtccagg 3538
295 ttgtccttga gtaataaaaa cgtatgttcc ctaaaaaaaa aaaaaggaat tc 3590
298 <210> SEQ ID NO: 5
299 <211> LENGTH: 712
300 <212> TYPE: PRT
301 <213> ORGANISM: Homo sapiens
303 <400> SEQUENCE: 5
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306 1 5 10 15
309 His Phe Leu Tyr Glu Val Pro Pro Trp Val Met Cys Arg Phe Tyr Lys
310 20 25 30
313 Val Met Asp Ala Leu Glu Pro Ala Asp Trp Cys Gln Phe Ala Ala Leu
314 35 40 45
317 Ile Val Arg Asp Gln Thr Glu Leu Arg Leu Cys Glu Arg Ser Gly Gln
318 50 55 60
321 Arg Thr Ala Ser Val Leu Trp Pro Trp Ile Asn Arg Asn Ala Arg Val
322 65 70 75 80
325 Ala Asp Leu Val His Ile Leu Thr His Leu Gln Leu Leu Arg Ala Arg
326 85 90 95
329 Asp Ile Ile Thr Ala Trp His Pro Pro Ala Pro Leu Pro Ser Pro Gly
330 100 105 110
333 Thr Thr Ala Pro Arg Pro Ser Ser Ile Pro Ala Pro Ala Glu Ala Glu
334 115 120 125
337 Ala Trp Ser Pro Arg Lys Leu Pro Ser Ser Ala Ser Thr Phe Leu Ser
338 130 135 140
341 Pro Ala Phe Pro Gly Ser Gln Thr His Ser Gly Pro Glu Leu Gly Leu
342 145 150 155 160
345 Val Pro Ser Pro Ala Ser Leu Trp Pro Pro Pro Pro Ser Pro Ala Pro
346 165 170 175
349 Ser Ser Thr Lys Pro Gly Pro Glu Ser Ser Val Ser Leu Leu Gln Gly
350 180 185 190
353 Ala Arg Pro Ser Pro Phe Cys Trp Pro Leu Cys Glu Ile Ser Arg Gly
354 195 200 205
357 Thr His Asn Phe Ser Glu Glu Leu Lys Ile Gly Glu Gly Gly Phe Gly
358 210 215 220
361 Cys Val Tyr Arg Ala Val Met Arg Asn Thr Val Tyr Ala Val Lys Arg

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<210> 29
<211> 20
<212> DNA
<213> Artificial
<220>
<223>
<400> 29
ccaaggtctc tagcactacc

Artificial

mandatory

20

if <213>
Response is Artificial/
Unknown, pls explain
in section <220> - <223>

See pg. 7 for
error explanation

↑
All types of errors shown exist throughout
the sequence listing. Please check subsequent
sequences for similar errors.

~~10/517,333~~

pts
insert

pls
explain

RAW SEQUENCE LISTING ERROR SUMMARY
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Input Set : A:\ISPT1011.ST25.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:13; N Pos. 625

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,3,6,7,8,9,10,11,16,17,18,19,20,21,22,23,24,25,26,27,28,31,32,33,34,35

Seq#:36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53,54,55,56,57,58,59

Seq#:60,61,62,63,64,65,66,67,68,69,70,71,72,73,74,75,76,77,78,80,81,82,83,84

Seq#:85,86

Use of <220> Feature (NEW RULES):

Sequence(s) are missing the <220> Feature and associated headings.

Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence" or "Unknown". Please explain source of genetic material in <220> to <223> section (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp.29631-32) (Sec.1.823 of new Rules)

Seq#:29,79

VERIFICATION SUMMARY

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Input Set : A:\ISPT1011.ST25.txt

Output Set: N:\CRF4\12222004\J517333.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1030 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:600
L:1235 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:29
L:1237 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:29, <213>
ORGANISM:Artificial Sequence
L:1237 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:29, <213>
ORGANISM:Artificial Sequence
L:1237 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:29,Line#:1237
L:1832 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:79
L:1834 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:79, <213>
ORGANISM:Artificial Sequence
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